

SEQUENCE LISTING

<110> Burgin, Alex B.
Stewart, Lance J.

<120> Use of Phosphorothiolate Polynucleotides
In Ligating Nucleic Acids

<130> P-RD 4806

<150> US 60/290,313
<151> 2001-05-10

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gtcacccgcg cttacctgcg cttccctcgag cttccggagt ccccggtccgc cccgacacaggc 180
cggttcgcgcg tctgegtctc ccccacgcgcg cctccgtctgc cgccgcgcgc gtcacctccgg 240
gcccac atg agt ggg gac cac aac gat tcc cag atc gaa gcg 288
Met Ser Gly Asp His Leu His Asn Asp Ser Gln Ile Glu Ala

1 5 10

gat ttc cga ttg aat gat tct cat aaa cac aaa gat aaa cac aaa gat 336
Asp Phe Arg Leu Asn Asp Ser His Lys His Lys Asp Lys His Lys Asp
15 20 25 30

cga gaa cac cgg cac aaa gaa cac aag aag gag aag gac cgg gaa aag 384
Arg Glu His Arg His Lys Glu His Lys Lys Glu Lys Asp Arg Glu Lys
35 40 45

tcc aag cat agc aac agt gaa cat aaa gat tct gaa aag aaa cac aaa 432
Ser Lys His Ser Asn Ser Glu His Lys Asp Ser Glu Lys Lys His Lys
50 55 60

gag aag gag aag acc aaa cac aaa gat gga agc tca gaa aag cat aaa 480
Glu Lys Glu Lys Thr Lys His Lys Asp Gly Ser Ser Glu Lys His Lys
65 70 75

gac aaa cat aaa gac aga gac aag gaa aaa cga aaa gag gaa aag gtt 528
Asp Lys His Lys Asp Arg Asp Lys Glu Lys Arg Lys Glu Glu Lys Val
80 85 90

cga gcc tct ggg gat gca aaa ata aag aag gag aag gaa aat ggc ttc 576
Arg Ala Ser Gly Asp Ala Lys Ile Lys Lys Glu Lys Glu Asn Gly Phe
95 100 105 110

tct agt cca cca caa att aaa gat gaa cct gaa gat gat ggc tat ttt 624
Ser Ser Pro Pro Gln Ile Lys Asp Glu Pro Glu Asp Asp Gly Tyr Phe
115 120 125

gtt cct cct aaa gag gat ata aag cca tta aag aga cct cga gat gag 672
Val Pro Pro Lys Glu Asp Ile Lys Pro Leu Lys Arg Pro Arg Asp Glu
130 135 140

gat gat gct gat tat aaa cct aag aaa att aaa aca gaa gat acc aag 720
Asp Asp Ala Asp Tyr Lys Pro Lys Lys Ile Lys Thr Glu Asp Thr Lys
145 150 155

aag gag aag aaa aga aaa cta gaa gaa gag gat ggt aaa ttg aaa 768
Lys Glu Lys Lys Arg Lys Leu Glu Glu Glu Asp Gly Lys Leu Lys
160 165 170

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Lys Pro Lys Asn Lys Asp Lys Asp Lys Val Pro Glu Pro Asp Asn
175 180 185 190

aag aaa aag aag ccg aag aaa gaa gag gaa cag aag tgg aaa tgg tgg 864
Lys Lys Lys Pro Lys Lys Glu Glu Gln Lys Trp Lys Trp Trp
195 200 205

gaa gaa gag cgc tat cct gaa ggc atc aag tgg aaa ttc cta gaa cat 912
Glu Glu Glu Arg Tyr Pro Glu Gly Ile Lys Trp Lys Phe Leu Glu His
210 215 220

aaa ggt cca gta ttt gcc cca cca tat gag cct ctt cca gag aat gtc 960
Lys Gly Pro Val Phe Ala Pro Pro Tyr Glu Pro Leu Pro Glu Asn Val
225 230 235

aag ttt tat tat gat ggt aaa gtc atg aag ctg agc ccc aaa gca gag 1008
Lys Phe Tyr Tyr Asp Gly Lys Val Met Lys Leu Ser Pro Lys Ala Glu
240 245 250

gaa gta gct acg ttc ttt gca aaa atg ctc gac cat gaa tat act acc 1056
Glu Val Ala Thr Phe Phe Ala Lys Met Leu Asp His Glu Tyr Thr Thr
255 260 265 270

aag gaa ata ttt agg aaa aat ttc ttt aaa gac tgg aga aag gaa atg 1104
Lys Glu Ile Phe Arg Lys Asn Phe Phe Lys Asp Trp Arg Lys Glu Met
275 280 285

act aat gaa gag aag aat att atc acc aac cta agc aaa tgt gat ttt 1152

Thr Asn Glu Glu Lys Asn Ile Ile Thr Asn Leu Ser Lys Cys Asp Phe
290 295 300 1200
acc cag atg agc cag tat ttc aaa gcc cag acg gaa gct cgg aaa cag
Thr Gln Met Ser Gln Tyr Phe Lys Ala Gln Thr Glu Ala Arg Lys Gln
305 310 315 1248
atg agc aag gaa gag aaa ctg aaa atc aaa gag gag aat gaa aaa tta
Met Ser Lys Glu Glu Lys Leu Lys Glu Glu Asn Glu Lys Leu
320 325 330 1296
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Leu Lys Glu Tyr Gly Phe Cys Ile Met Asp Asn His Lys Glu Arg Ile
335 340 345 350 1344
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Ala Asn Phe Lys Ile Glu Pro Pro Gly Leu Phe Arg Gly Arg Gly Asn
355 360 365 1392
cac ccc aag atg ggc atg ctg aag aga cga atc atg ccc gag gat ata
His Pro Lys Met Gly Met Leu Lys Arg Arg Ile Met Pro Glu Asp Ile
370 375 380 1440
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Ile Ile Asn Cys Ser Lys Asp Ala Lys Val Pro Ser Pro Pro Gly
385 390 395 1488
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His Lys Trp Lys Glu Val Arg His Asp Asn Lys Val Thr Trp Leu Val
400 405 410 1536
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Ser Trp Thr Glu Asn Ile Gln Gly Ser Ile Lys Tyr Ile Met Leu Asn
415 420 425 430 1584
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Ala Arg Arg Leu Lys Lys Cys Val Asp Lys Ile Arg Asn Gln Tyr Arg
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Glu Asp Trp Lys Ser Lys Glu Met Lys Val Arg Gln Arg Ala Val Ala
465 470 475 1728
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Leu Tyr Phe Ile Asp Lys Leu Ala Leu Arg Ala Gly Asn Glu Lys Glu
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His Ile Asn Leu His Pro Glu Leu Asp Gly Gln Glu Tyr Val Val Glu				
515		520		525
ttt gac ttc ctc ggg aag gac tcc atc aga tac tat aac aag gtc cct				1872
Phe Asp Phe Leu Gly Lys Asp Ser Ile Arg Tyr Tyr Asn Lys Val Pro				
530		535		540
gtt gag aaa cga gtt ttt aag aac cta caa cta ttt atg gag aac aag				1920
Val Glu Lys Arg Val Phe Lys Asn Leu Gln Leu Phe Met Glu Asn Lys				
545		550		555
cag ccc gag gat gat ctt ttt gat aga ctc aat act ggt att ctg aat				1968
Gln Pro Glu Asp Asp Leu Phe Asp Arg Leu Asn Thr Gly Ile Leu Asn				
560		565		570
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Lys His Leu Gln Asp Leu Met Glu Gly Leu Thr Ala Lys Val Phe Arg				
575		580		590
aca tac aat gcc tcc atc acg cta cag cag cta aaa gaa ctg aca				2064
Thr Tyr Asn Ala Ser Ile Thr Leu Gln Gln Leu Lys Glu Leu Thr				
595		600		605
gcc ccg gat gag aac atc cca gcg aag atc ctt tct tat aac cgt gcc				2112
Ala Pro Asp Glu Asn Ile Pro Ala Lys Ile Leu Ser Tyr Asn Arg Ala				
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aat cga gct gtt gca att ctt tgt aac cat cag agg gca cca cca aaa				2160
Asn Arg Ala Val Ala Ile Leu Cys Asn His Gln Arg Ala Pro Pro Lys				
625		630		635
act ttt gag aag tct atg atg aac ttg caa act aag att gat gcc aag				2208
Thr Phe Glu Lys Ser Met Met Asn Leu Gln Thr Lys Ile Asp Ala Lys				
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Lys Glu Gln Leu Ala Asp Ala Arg Arg Asp Leu Lys Ser Ala Lys Ala				
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Asp Ala Lys Val Met Lys Asp Ala Lys Thr Lys Val Val Glu Ser				
675		680		685
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Lys Trp Gly Val Pro Ile Glu Lys Ile Tyr Asn Lys Thr Gln Arg Glu
735 740 750

aag ttt gcc tgg gcc att gac atg gct gat gaa gac tat gag ttt 2541
Lys Phe Ala Trp Ala Ile Asp Met Ala Asp Glu Asp Tyr Glu Phe
755 760 765

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His Arg His Lys Glu His Lys Lys Glu Lys Asp Arg Glu Lys Ser Lys
35 40 45
His Ser Asn Ser Glu His Lys Asp Ser Glu Lys Lys His Lys Glu Lys
50 55 60
Glu Lys Thr Lys His Lys Asp Gly Ser Ser Glu Lys His Lys Asp Lys
65 70 75 80
His Lys Asp Arg Asp Lys Glu Lys Arg Lys Glu Glu Lys Val Arg Ala
85 90 95
Ser Gly Asp Ala Lys Ile Lys Lys Glu Lys Glu Asn Gly Phe Ser Ser

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Pro Pro Gln Ile Lys Asp Glu Pro Glu Asp Asp Gly Tyr Phe Val Pro		
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Pro Lys Glu Asp Ile Lys Pro Leu Lys Arg Pro Arg Asp Glu Asp Asp		
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Ala Asp Tyr Lys Pro Lys Lys Ile Lys Thr Glu Asp Thr Lys Lys Glu		
145	150	155
Lys Lys Arg Lys Leu Glu Glu Glu Asp Gly Lys Leu Lys Lys Pro		
165	170	175
Lys Asn Lys Asp Lys Asp Lys Lys Val Pro Glu Pro Asp Asn Lys Lys		
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Lys Lys Pro Lys Lys Glu Glu Gln Lys Trp Lys Trp Trp Glu Glu		
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Glu Arg Tyr Pro Glu Gly Ile Lys Trp Lys Phe Leu Glu His Lys Gly		
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Pro Val Phe Ala Pro Pro Tyr Glu Pro Leu Pro Glu Asn Val Lys Phe		
225	230	235
Tyr Tyr Asp Gly Lys Val Met Lys Leu Ser Pro Lys Ala Glu Glu Val		
245	250	255
Ala Thr Phe Phe Ala Lys Met Leu Asp His Glu Tyr Thr Thr Lys Glu		
260	265	270
Ile Phe Arg Lys Asn Phe Phe Lys Asp Trp Arg Lys Glu Met Thr Asn		
275	280	285
Glu Glu Lys Asn Ile Ile Thr Asn Leu Ser Lys Cys Asp Phe Thr Gln		
290	295	300
Met Ser Gln Tyr Phe Lys Ala Gln Thr Glu Ala Arg Lys Gln Met Ser		
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Lys Glu Glu Lys Leu Lys Ile Lys Glu Glu Asn Glu Lys Leu Lys		
325	330	335
Glu Tyr Gly Phe Cys Ile Met Asp Asn His Lys Glu Arg Ile Ala Asn		
340	345	350
Phe Lys Ile Glu Pro Pro Gly Leu Phe Arg Gly Arg Gly Asn His Pro		
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Lys Met Gly Met Leu Lys Arg Arg Ile Met Pro Glu Asp Ile Ile Ile		
370	375	380
Asn Cys Ser Lys Asp Ala Lys Val Pro Ser Pro Pro Pro Gly His Lys		
385	390	395
Trp Lys Glu Val Arg His Asp Asn Lys Val Thr Trp Leu Val Ser Trp		
405	410	415
Thr Glu Asn Ile Gln Gly Ser Ile Lys Tyr Ile Met Leu Asn Pro Ser		
420	425	430
Ser Arg Ile Lys Gly Glu Lys Asp Trp Gln Lys Tyr Glu Thr Ala Arg		
435	440	445
Arg Leu Lys Lys Cys Val Asp Lys Ile Arg Asn Gln Tyr Arg Glu Asp		
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Trp Lys Ser Lys Glu Met Lys Val Arg Gln Arg Ala Val Ala Leu Tyr		
465	470	475
Phe Ile Asp Lys Leu Ala Leu Arg Ala Gly Asn Glu Lys Glu Glu Gly		
485	490	495
Glu Thr Ala Asp Thr Val Gly Cys Cys Ser Leu Arg Val Glu His Ile		
500	505	510
Asn Leu His Pro Glu Leu Asp Gly Gln Glu Tyr Val Val Glu Phe Asp		
515	520	525

Phe Leu Gly Lys Asp Ser Ile Arg Tyr Tyr Asn Lys Val Pro Val Glu
530 535 540
Lys Arg Val Phe Lys Asn Leu Gln Leu Phe Met Glu Asn Lys Gln Pro
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Glu Asp Asp Leu Phe Asp Arg Leu Asn Thr Gly Ile Leu Asn Lys His
565 570 575
Leu Gln Asp Leu Met Glu Gly Leu Thr Ala Lys Val Phe Arg Thr Tyr
580 585 590
Asn Ala Ser Ile Thr Leu Gln Gln Leu Lys Glu Leu Thr Ala Pro
595 600 605
Asp Glu Asn Ile Pro Ala Lys Ile Leu Ser Tyr Asn Arg Ala Asn Arg
610 615 620
Ala Val Ala Ile Leu Cys Asn His Gln Arg Ala Pro Pro Lys Thr Phe
625 630 635 640
Glu Lys Ser Met Met Asn Leu Gln Thr Lys Ile Asp Ala Lys Lys Glu
645 650 655
Gln Leu Ala Asp Ala Arg Arg Asp Leu Lys Ser Ala Lys Ala Asp Ala
660 665 670
Lys Val Met Lys Asp Ala Lys Thr Lys Lys Val Val Glu Ser Lys Lys
675 680 685
Lys Ala Val Gln Arg Leu Glu Glu Gln Leu Met Lys Leu Glu Val Gln
690 695 700
Ala Thr Asp Arg Glu Glu Asn Lys Gln Ile Ala Leu Gly Thr Ser Lys
705 710 715 720
Leu Asn Tyr Leu Asp Pro Arg Ile Thr Val Ala Trp Cys Lys Lys Trp
725 730 735
Gly Val Pro Ile Glu Lys Ile Tyr Asn Lys Thr Gln Arg Glu Lys Phe
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<221> CDS
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His Ile Glu Gly Arg Ile Lys Trp Lys Phe Leu Glu His Lys Gly Pro
20 25 30

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Val Phe Ala Pro Pro Tyr Glu Pro Leu Pro Glu Asn Val Lys Phe Tyr			
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tat gat ggt aaa gtc atg aag ctg agc ccc aaa gca gag gaa gta gct			192
Tyr Asp Gly Lys Val Met Lys Leu Ser Pro Lys Ala Glu Glu Val Ala			
50	55	60	
acg ttc ttt gca aaa atg ctc gac cat gaa tat act acc aag gaa ata			240
Thr Phe Phe Ala Lys Met Leu Asp His Glu Tyr Thr Thr Lys Glu Ile			
65	70	75	80
ttt agg aaa aat ttc ttt aaa gac tgg aga aag gaa atg act aat gaa			288
Phe Arg Lys Asn Phe Phe Lys Asp Trp Arg Lys Glu Met Thr Asn Glu			
85	90	95	
gag aag aat att atc acc aac cta agc aaa tgt gat ttt acc cag atg			336
Glu Lys Asn Ile Ile Thr Asn Leu Ser Lys Cys Asp Phe Thr Gln Met			
100	105	110	
agc cag tat ttc aaa gcc cag acg gaa gct cggt aaa cag atg agc aag			384
Ser Gln Tyr Phe Lys Ala Gln Thr Glu Ala Arg Lys Gln Met Ser Lys			
115	120	125	
gaa gag aaa ctg aaa atc aaa gag gag aat gaa aaa tta ctg aaa gaa			432
Glu Glu Lys Leu Lys Ile Lys Glu Glu Asn Glu Lys Leu Leu Lys Glu			
130	135	140	
tat gga ttc tgt att atg gat aac cac aaa gag agg att gct aac ttc			480
Tyr Gly Phe Cys Ile Met Asp Asn His Lys Glu Arg Ile Ala Asn Phe			
145	150	155	160
aag ata gag cct cct gga ctt ttc cgt ggc cgc ggc aac cac ccc aag			528
Lys Ile Glu Pro Pro Gly Leu Phe Arg Gly Arg Gly Asn His Pro Lys			
165	170	175	
atg ggc atg ctg aag aga cga atc atg ccc gag gat ata atc atc aac			576
Met Gly Met Leu Lys Arg Arg Ile Met Pro Glu Asp Ile Ile Ile Asn			
180	185	190	
tgt agc aaa gat gcc aag gtt cct tct cct cca gga cat aag tgg			624
Cys Ser Lys Asp Ala Lys Val Pro Ser Pro Pro Gly His Lys Trp			
195	200	205	
aaa gaa gtc cgg cat gat aac aag gtt act tgg ctg gtt tcc tgg aca			672
Lys Glu Val Arg His Asp Asn Lys Val Thr Trp Leu Val Ser Trp Thr			
210	215	220	
gag aac atc caa ggt tcc att aaa tac atc atg ctt aac cct agt tca			720
Glu Asn Ile Gln Gly Ser Ile Lys Tyr Ile Met Leu Asn Pro Ser Ser			
225	230	235	240
cga atc aag ggt gag aag gac tgg cag aaa tac gag act gct cgg cgg			768
Arg Ile Lys Gly Glu Lys Asp Trp Gln Lys Tyr Glu Thr Ala Arg Arg			

245	250	255	
ctg aaa aaa tgt gtg gac aag atc cg ^g aac cag tat cga gaa gac tgg Leu Lys Lys Cys Val Asp Lys Ile Arg Asn Gln Tyr Arg Glu Asp Trp 260	265	270	816
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aca gcg gac act gtg ggc tgc tgc tca ctt cgt gtg qag cac atc aat Thr Ala Asp Thr Val Gly Cys Ser Leu Arg Val Glu His Ile Asn 305	310	315	960
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ctc ggg aag gac tcc atc aga tac tat aac aag gtc cct gtt gag aaa Leu Gly Lys Asp Ser Ile Arg Tyr Tyr Asn Lys Val Pro Val Glu Lys 340	345	350	1056
cga gtt ttt aag aac cta caa cta ttt atg gag aac aag cag ccc gag Arg Val Phe Lys Asn Leu Gln Leu Phe Met Glu Asn Lys Gln Pro Glu 355	360	365	1104
gat gat ctt ttt gat aga ctc aat act ggt att ctg aat aag cat ctt Asp Asp Leu Phe Asp Arg Leu Asn Thr Gly Ile Leu Asn Lys His Leu 370	375	380	1152
cag gat ctc atg gag ggc ttg aca gcc aag gta ttc cgt acg tac aat Gln Asp Leu Met Glu Gly Leu Thr Ala Lys Val Phe Arg Thr Tyr Asn 385	390	395	1200
gcc tcc atc acg cta cag cag cta aaa gaa ctg aca gcc ccg gat Ala Ser Ile Thr Leu Gln Gln Leu Lys Glu Leu Thr Ala Pro Asp 405	410	415	1248
gag aac atc cca gcg aag atc ctt tct tat aac cgt gcc aat cga gct Glu Asn Ile Pro Ala Lys Ile Leu Ser Tyr Asn Arg Ala Asn Arg Ala 420	425	430	1296
gtt gca att ctt tgt aac cat cag agg gca cca cca aaa act ttt gag Val Ala Ile Leu Cys Asn His Gln Arg Ala Pro Pro Lys Thr Phe Glu 435	440	445	1344
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cta gca gat gcc cgg aga gac ctg aaa agt gct aag gct gat gcc aag 1440
Leu Ala Asp Ala Arg Arg Asp Leu Lys Ser Ala Lys Ala Asp Ala Lys
465 470 475 480

gtc atg aag gat gca aag acg aag aag gta gta gag tca aag aag aag 1488
Val Met Lys Asp Ala Lys Thr Lys Lys Val Val Glu Ser Lys Lys Lys
485 490 495

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Ala Val Gln Arg Leu Glu Glu Gln Leu Met Lys Leu Glu Val Gln Ala
500 505 510

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Thr Asp Arg Glu Glu Asn Lys Gln Ile Ala Leu Gly Thr Ser Lys Leu
515 520 525

aat tat ctg gac cct agg atc aca gtg gct tgg tgc aag aag tgg ggt 1632
Asn Tyr Leu Asp Pro Arg Ile Thr Val Ala Trp Cys Lys Lys Trp Gly
530 535 540

gtc cca att gag aag att tac aac aaa acc cag cgg gag aag ttt gcc 1680
Val Pro Ile Glu Lys Ile Tyr Asn Lys Thr Gln Arg Glu Lys Phe Ala
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35 40 45
Tyr Asp Gly Lys Val Met Lys Leu Ser Pro Lys Ala Glu Glu Val Ala
50 55 60
Thr Phe Phe Ala Lys Met Leu Asp His Glu Tyr Thr Thr Lys Glu Ile
65 70 75 80
Phe Arg Lys Asn Phe Phe Lys Asp Trp Arg Lys Glu Met Thr Asn Glu
85 90 95
Glu Lys Asn Ile Ile Thr Asn Leu Ser Lys Cys Asp Phe Thr Gln Met
100 105 110

Ser Gln Tyr Phe Lys Ala Gln Thr Glu Ala Arg Lys Gln Met Ser Lys
115 120 125
Glu Glu Lys Leu Lys Ile Lys Glu Glu Asn Glu Lys Leu Leu Lys Glu
130 135 140
Tyr Gly Phe Cys Ile Met Asp Asn His Lys Glu Arg Ile Ala Asn Phe
145 150 155 160
Lys Ile Glu Pro Pro Gly Leu Phe Arg Gly Arg Gly Asn His Pro Lys
165 170 175
Met Gly Met Leu Lys Arg Arg Ile Met Pro Glu Asp Ile Ile Asn
180 185 190
Cys Ser Lys Asp Ala Lys Val Pro Ser Pro Pro Gly His Lys Trp
195 200 205
Lys Glu Val Arg His Asp Asn Lys Val Thr Trp Leu Val Ser Trp Thr
210 215 220
Glu Asn Ile Gln Gly Ser Ile Lys Tyr Ile Met Leu Asn Pro Ser Ser
225 230 235 240
Arg Ile Lys Gly Glu Lys Asp Trp Gln Lys Tyr Glu Thr Ala Arg Arg
245 250 255
Leu Lys Lys Cys Val Asp Lys Ile Arg Asn Gln Tyr Arg Glu Asp Trp
260 265 270
Lys Ser Lys Glu Met Lys Val Arg Gln Arg Ala Val Ala Leu Tyr Phe
275 280 285
Ile Asp Lys Leu Ala Leu Arg Ala Gly Asn Glu Lys Glu Glu Gly Glu
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Thr Ala Asp Thr Val Gly Cys Ser Leu Arg Val Glu His Ile Asn
305 310 315 320
Leu His Pro Glu Leu Asp Gly Gln Glu Tyr Val Val Glu Phe Asp Phe
325 330 335
Leu Gly Lys Asp Ser Ile Arg Tyr Tyr Asn Lys Val Pro Val Glu Lys
340 345 350
Arg Val Phe Lys Asn Leu Gln Leu Phe Met Glu Asn Lys Gln Pro Glu
355 360 365
Asp Asp Leu Phe Asp Arg Leu Asn Thr Gly Ile Leu Asn Lys His Leu
370 375 380
Gln Asp Leu Met Glu Gly Leu Thr Ala Lys Val Phe Arg Thr Tyr Asn
385 390 395 400
Ala Ser Ile Thr Leu Gln Gln Leu Lys Glu Leu Thr Ala Pro Asp
405 410 415
Glu Asn Ile Pro Ala Lys Ile Leu Ser Tyr Asn Arg Ala Asn Arg Ala
420 425 430
Val Ala Ile Leu Cys Asn His Gln Arg Ala Pro Pro Lys Thr Phe Glu
435 440 445
Lys Ser Met Met Asn Leu Gln Thr Lys Ile Asp Ala Lys Lys Glu Gln
450 455 460
Leu Ala Asp Ala Arg Arg Asp Leu Lys Ser Ala Lys Ala Asp Ala Lys
465 470 475 480
Val Met Lys Asp Ala Lys Thr Lys Lys Val Val Glu Ser Lys Lys Lys
485 490 495
Ala Val Gln Arg Leu Glu Glu Gln Leu Met Lys Leu Glu Val Gln Ala
500 505 510
Thr Asp Arg Glu Glu Asn Lys Gln Ile Ala Leu Gly Thr Ser Lys Leu
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Asn Tyr Leu Asp Pro Arg Ile Thr Val Ala Trp Cys Lys Lys Trp Gly

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